AMENDMENT TO THE SPECIFICATION

Please amend the specification as follows:

Please replace the paragraph spanning line 29, page 24, to line 6, page 26 (paragraph [0114] of U.S. publication 20030049815), with the following amended paragraph.

A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequence for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482, 1981, by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol 48:443, 1970, by the search for similarity method of person & Lipman, Proc. Nat'l. Acad. Sci. USA 85:2444, 1988, by computerized implementations of these algorithms (GAP™, BESTFIT™, FASTA™, and TFASTA™ in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by manual alignment and visual inspection. Other algorithms for determining homology or identity include, for example, in addition to a BLAST program (Basic Local Alignment Search Tool at the National Center for Biological Information), ALIGN™, AMAS™ (Analysis of Multiply Aligned Sequences), AMPS™ (Protein Multiple Sequence Alignment), ASSET™ (Aligned Segment Statistical Evaluation Tool), BANDS™, BESTSCOR™, BIOSCAN™ (Biological Sequence Comparative Analysis Node), BLIMPS™ (BLocks IMProved Searcher), FASTA™, Intervals & Points, BMB™, CLUSTAL V™, CLUSTAL W™, CONSENSUS™, LCONSENSUS™, WCONSENSUS™, Smith-Waterman algorithm, DARWIN™, Las Vegas algorithm, FNAT™ (Forced Nucleotide Alignment Tool), Framealign, Framesearch, DYNAMIC, FILTER, FSAP (Fristensky Sequence Analysis Package), GAP (Global Alignment Program), GENAL™, GIBBS™, GenQuest, ISSC™ (Sensitive Sequence Comparison), LALIGN™ (Local Sequence Alignment), LCP™ (Local Content Program), MACAW™ (Multiple Alignment Construction & Analysis Workbench), MAP™ (Multiple Alignment Program), MBLKP™, MBLKN™, PIMA™ (Pattern-

Induced Multi-sequence Alignment), SAGA™ (Sequence Alignment by Genetic Algorithm) and WHAT-IF™. Such alignment programs can also be used to screen genome databases to identify polynucleotide sequences having substantially identical sequences. A number of genome databases are available, for example, a substantial portion of the human genome is available as part of the Human Genome Sequencing Project ~~(J. Roach, http://weber.u.Washington.edu/.about.roach/human_genome_progress2.html) (Gibbs, 1995)~~. At least twenty-one other genomes have already been sequenced, including, for example, M. genitalium (Fraser et al., 1995), M. jannaschii (Bult et al., 1996), H. influenzae (Fleischmann et al., 1995), E. coli (Blattner et al., 1997), and yeast (S. cerevisiae) (Mewes et al., 1997), and D. melanogaster (Adams et al., 2000). Significant progress has also been made in sequencing the genomes of model organism, such as mouse, C. elegans, and Arabadopsis sp. Several databases containing genomic information annotated with some functional information are maintained by different organization, and are accessible via the internet~~, for example, http://wwwtigr.org/tdb; http://www.genetics.wisc.edu; http://genome-www.stanford.edu/.about.ball; http://hiv-web.lanl.gov; http://www.ncbi.nlm.nih.gov; http://www.ebi.ac.uk; http://Pasteur.fr/other/biology; and http://www.genome.wi.mit.edu~~.

Please replace the paragraph spanning lines 7 to 31, page 26 (paragraph [0115] of U.S. publication 20030049815), with the following amended paragraph.

One example of a useful algorithm is BLAST™ and BLAST 2.0™ algorithms, which are described in Altschul et al., Nuc. Acids Res. 25:3389-3402, 1977, and Altschul et al., J. Mol. Biol. 215:403-410, 1990, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/)~~. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score

for a pair of matching residues; always >0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST™ algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN™ program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP™ program uses as defaults a wordlength of 3, and expectations (E) of 10, and the BLOSUM62™ scoring matrix (see Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89:10915, 1989) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Please replace the paragraph spanning line 31, page 43, to line 13, page 44 (paragraph [0194] of U.S. publication 20030049815), with the following amended paragraph.

As representative examples of expression vectors which may be used there may be mentioned viral particles, baculovirus, phage, plasmids, phagemids, cosmids, fosmids, bacterial artificial chromosomes, viral DNA (e.g., vaccinia, adenovirus, foul pox virus, pseudorabies and derivatives of SV40), P1-based artificial chromosomes, yeast plasmids, yeast artificial chromosomes, and any other vectors specific for specific hosts of interest (such as bacillus, aspergillus and yeast). Thus, for example, the DNA may be included in any one of a variety of expression vectors for expressing a polypeptide. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences. Large numbers of suitable vectors are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example; Bacterial: pQE™ vectors (Qiagen), pBLUESCRIPT™ ~~pBluescript~~ plasmids, pNH™ vectors, (lambda-ZAP™ vectors (Stratagene); ptrc99a, pKK223-3™, pDR540™, pRIT2T™ (Pharmacia); Eukaryotic: pXT1™, pSG5™ (Stratagene), pSVK3™, pBPV™, pMSG™, pSVLSV40™ (Pharmacia). However, any other plasmid or other vector may be used so long as they are replicable and viable in the host. Low copy number or high copy number vectors may be employed with the present invention.

Please replace the paragraph spanning lines 1 to 5, page 44 (paragraph [0241] of U.S. publication 20030049815), with the following amended paragraph.

PCR product and pQE60™ vector (Qiagen) were both digested with EcoRI and BglII restriction endonucleases (New England Biolabs) according to manufacturers protocols. Ligation and transformation into, and expression in M15 pREP4™ host cells (Qiagen) yields c-term 6X-His tagged protein.

Please replace the paragraph spanning lines 9 to 13, page 59 (paragraph [0262] of U.S. publication 20030049815), with the following amended paragraph.

The following vectors are provided by way of example; Bacterial: pQE70™, pQE60™, pQE-9™ (Qiagen), pBLUESCRIPT II™ ~~pBluescript II~~ (Stratagene); pTRC99a™, pKK223-3™, pDR540™, pRIT2T™ (Pharmacia); Eukaryotic: pXTI™, pSG5™ (Stratagene) pSVK3™, pBPV™, pMSG™, pSVLSV40™ (Pharmacia). However, any other plasmids or other vectors may be used as long as they are replicable and viable in the host.

Please replace the paragraph spanning lines 6 to 12, page 61 (paragraph [0271] of U.S. publication 20030049815), with the following amended paragraph.

As a representative but nonlimiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3™ (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEMI™ (Promega Biotec, Madison, Wis., USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Please replace the paragraph spanning lines 7 to 14, page 96 (paragraph [0402] of U.S. publication 20030049815), with the following amended paragraph.

In another embodiment, a digestive aid containing an enzyme either as the sole active ingredient or in combination with one or more other agents and/or enzymes is provided (as described in co-pending application U.S. Ser. No. 09/580,515, entitled "Dietary Aids and Methods of Use Thereof," filed May 25, 2000 (issued as USPN 6,720,014, April 13, 2004), the disclosure of which is incorporated herein by reference in its entirety). The use of enzymes and other agents in digestive aids of livestock or domesticated animals not only improves the animal's health and life expectancy but also assists in increasing the health of livestock and in the production of foodstuffs from livestock.